

QY 121 CTGCGCGATGCTTTATAGAGAGGTTGGTCAGCATCGATCTCTGCCAGTGCTAGCTGA 180
Db |||||
QY 121 CTGCGCGATGCTTTATAGAGAGGTTGGTCAGCATCGATCTCTGCCAGTGCTAGCTGA 180
Db |||||
QY 181 GAACATG 187
Db 181 GAACATG 187

RESULT 2

US-10-058-566-5
; Sequence 5, Application US/10058566
; Publication No. US20020183274A1
; GENERAL INFORMATION:
; APPLICANT: ALBERTSEN, MARC
; APPLICANT: FOX, TIM
; APPLICANT: HUFFMAN, GARY
; APPLICANT: TRIMMELL, MARY
; TITLE OF INVENTION: NUCLEOTIDE SEQUENCES MEDIATING MALE FERTILITY AND
; FILE REFERENCE: METHOD OF USING SAME
; CURRENT APPLICATION NUMBER: US/10/058,566
; CURRENT FILING DATE: 2002-01-28
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 322
; TYPE: DNA
; ORGANISM: Zea mays
US-10-058-566-5

Query Match 100.0%; Score 187; DB 13; Length 322;
Best Local Similarity 100.0%; Pred. No. 4.4e-53;
Matches 187; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGCGTCTCGATCGATTGCAAAATCTACCTCCAAACCAACCCAGCTTTGTATCTGCTTACTG 60
Db 136 CGCGTCTCGATCGATTGCAAAATCTACCTCCAAACCAACCCAGCTTTGTATCTGCTTACTG 195
QY 61 TGATCACCACCAAGTTGCTGATACGATGTGCGATTATTGCTCTTTCTCTCTAGAAATGTT 120
Db 196 TGATCACCACCAAGTTGCTGATACGATGTGCGATTATTGCTCTTTCTCTCTAGAAATGTT 255
QY 121 CTGCGCGATGCTTTATAGAGAGGTTGGTCAGCATCGATCTCTGCCAGTGCTAGCTGA 180
Db 256 CTGCGCGATGCTTTATAGAGAGGTTGGTCAGCATCGATCTCTGCCAGTGCTAGCTGA 315
QY 181 GAACATG 187
Db 316 GAACATG 322

RESULT 3

US-10-058-566-3
; Sequence 3, Application US/10058566
; Publication No. US20020183274A1
; GENERAL INFORMATION:
; APPLICANT: ALBERTSEN, MARC
; APPLICANT: FOX, TIM
; APPLICANT: HUFFMAN, GARY
; APPLICANT: TRIMMELL, MARY
; TITLE OF INVENTION: NUCLEOTIDE SEQUENCES MEDIATING MALE FERTILITY AND
; FILE REFERENCE: METHOD OF USING SAME
; CURRENT APPLICATION NUMBER: US/10/058,566
; CURRENT FILING DATE: 2002-01-28
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 2544
; TYPE: DNA
; ORGANISM: Zea mays
US-10-058-566-3

Query Match 100.0%; Score 187; DB 13; Length 2544;
Best Local Similarity 100.0%; Pred. No. 1e-52;
Matches 187; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CGCGTCTCGATCGATTGCAAAATCTACCTCCAAACCAACCCAGCTTTGTATCTGCTTACTG 60
Db 136 CGCGTCTCGATCGATTGCAAAATCTACCTCCAAACCAACCCAGCTTTGTATCTGCTTACTG 195
QY 61 TGATCACCACCAAGTTGCTGATACGATGTGCGATTATTGCTCTTTCTCTCTAGAAATGTT 120
Db 196 TGATCACCACCAAGTTGCTGATACGATGTGCGATTATTGCTCTTTCTCTCTAGAAATGTT 255
QY 121 CTGCGCGATGCTTTATAGAGAGGTTGGTCAGCATCGATCTCTGCCAGTGCTAGCTGA 180
Db 256 CTGCGCGATGCTTTATAGAGAGGTTGGTCAGCATCGATCTCTGCCAGTGCTAGCTGA 315
QY 181 GAACATG 187
Db 316 GAACATG 322

RESULT 4

US-10-260-238-2894
; Sequence 2894, Application US/10260238
; Publication No. US20040016025A1
; GENERAL INFORMATION:
; APPLICANT: Budworth, Paul R.
; APPLICANT: Moughamer, Todd G.
; APPLICANT: Briggs, Steven P.
; APPLICANT: Cooper, Bret
; APPLICANT: Glazebrook, Jane
; APPLICANT: Goff, Stephen A.
; APPLICANT: Katagiri, Fumiaki
; APPLICANT: Kreps, Joel
; APPLICANT: Provart, Nicholas
; APPLICANT: Rieke, Darrell
; APPLICANT: Zhu, Tong
; TITLE OF INVENTION: PROMOTERS FOR REGULATION OF PLANT EXPRESSION
; FILE REFERENCE: 6011-NP
; CURRENT APPLICATION NUMBER: US/10/260,238
; CURRENT FILING DATE: 2002-09-26
; PRIOR APPLICATION NUMBER: US 60/325,448
; PRIOR FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: US 60/325,277
; PRIOR FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: US 60/370,620
; PRIOR FILING DATE: 2002-04-04
; NUMBER OF SEQ ID NOS: 6077
; SEQ ID NO 2894
; LENGTH: 714
; TYPE: DNA
; ORGANISM: Triticum aestivum
US-10-260-238-2894

Query Match 23.4%; Score 43.8; DB 17; Length 714;
Best Local Similarity 63.9%; Pred. No. 0.0003;
Matches 99; Conservative 0; Mismatches 52; Indels 4; Gaps 2;
QY 5 TCCTGGATCGATTGCAAAATCTACCTCCAAACCAACCCAGCTTTGTATCTGCTTACTGTGAT 64
Db 432 TTCAGATGTACTGTAAATCTGCAATTCACCAACCCAGCTTTGACCTGTTAATAACTGT 491
QY 65 CACCAAGTTGCTGTATACGATGTGCGATTATTGCTCTTTCTCTCTAGAAATGTTCTGT 124
Db 492 GATCACAAAATGGG---TGATGAACCATTTTGGATCCTCTCTCTAGAAATGTTCTTT 548
QY 125 CCGATGCTTTATAGAGAGGTTGGTCAGCATCGA 159
Db 549 GACGTGC-TTATATAGAGAGCTGGATTTCGCTCAA 582

RESULT 5

US-09-070-927A-550/G
; Sequence 550, Application US/09070927A
; Patent No. US20020120116A1
; GENERAL INFORMATION:
; APPLICANT: Charles A. Kunesch
; Patrick J. Dillon
; Steven Barash
; TITLE OF INVENTION: Enterococcus faecialis Polynucleotides and Polypeptides
; NUMBER OF SEQUENCES: 982
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/070,927A
; FILING DATE: 04-May-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/046,655
; FILING DATE: 1997-05-16
; APPLICATION NUMBER: 60/044,031
; FILING DATE: 1997-05-06
; APPLICATION NUMBER: 60/066,009
; FILING DATE: 1997-11-14
; ATTORNEY/AGENT INFORMATION:
; NAME: Kenley K. Hoover
; REGISTRATION NUMBER: 40,302
; REFERENCE/DOCKET NUMBER: PB369
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 550:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9797 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 550:
US-09-070-927A-550
Query Match 17.9%; Score 33.4; DB 9; Length 9797;
Best Local Similarity 52.5%; Pred. No. 3;
Matches 73; Conservative 0; Mismatches 66; Indels 0; Gaps 0;
Qy 8 TGGATCGATTGCAATCTACCTCCCAACCAACCCAGCTTGTATCTGCTTACTGTGATCAC 67
Db 4260 TGGAAACGATTGTCACACTATCCCAACAAACATGTCATTAGGTTGATTTTCAGATAACGG 4201
Qy 68 CAAAGTTGTGCTGATACGATGCGGATTATGCTCTTCTCTCTAGAAATGTTCTCGCG 127
Db 4200 CACAGAATTATTGATTCATATTGGATTGATACAGTTCAATTAGAACGCGAGCCTTGA 4141
Qy 128 ATGCTTTTATAAGAAAGT 146
Db 4140 AGCTTTTGTAAACAAGT 4122
RESULT 6
US-10-424-599-77478
; Sequence 77478, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua

; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 77478
; LENGTH: 533
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_40980C.1
US-10-424-599-77478
Query Match 17.3%; Score 32.4; DB 17; Length 533;
Best Local Similarity 54.1%; Pred. No. 2;
Matches 66; Conservative 0; Mismatches 56; Indels 0; Gaps 0;
Qy 24 CTACCTCCAAACCAACCCAGCTTTGTATCTGCTTACTGTGATCACCACAAAGTTGTGCTGATA 83
Db 253 CTGCTTCCATCTTCCCATCATGCTCATGCCCTGGAAATGGGATTTCACCTTGGCTGATT 312
Qy 84 CGATGCGGATTATTGCTCTTTCTTCTCTAGAAATGTTCTGCGCATGCTTTTATAAGAGAA 143
Db 313 TCGTCATGCGCTTTTCTTTTTCATTGCTGGAATTTCTTGGCCCTCGTTTATAAGAGAA 372
Qy 144 GG 145
Db 373 GG 374
RESULT 7
US-10-322-696-79
; Sequence 79, Application US/10322696
; Publication No. US20040166490A1
; GENERAL INFORMATION:
; APPLICANT: Morris, David W.
; APPLICANT: Malandro, Marc
; TITLE OF INVENTION: NOVEL THERAPEUTIC TARGETS IN CANCER
; FILE REFERENCE: 529452001200
; CURRENT APPLICATION NUMBER: US/10/322,696
; CURRENT FILING DATE: 2003-10-17
; NUMBER OF SEQ ID NOS: 186
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 79
; LENGTH: 352938
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)-(352938)
; OTHER INFORMATION: n = A,T,C or G
US-10-322-696-79
Query Match 16.9%; Score 31.6; DB 18; Length 352938;
Best Local Similarity 62.8%; Pred. No. 54;
Matches 49; Conservative 0; Mismatches 29; Indels 0; Gaps 0;
Qy 110 TCTAGAAATGTTCTGCGCATGCTTTTATAAGAAAGTTGTTGTCAGCATCGATCTCTGCCAG 169
Db 319069 TTTAGTATGCAACCGCGCATGGCTTGGAGGACAATGATGCTCAGCCCTAAATCTTAGCCAT 319128
Qy 170 TGCTAGCTGGAACATG 187
Db 319129 TTTCTCACTTTGGACAAG 319146
RESULT 8
US-10-072-077A-1/C
; Sequence 1, Application US/10072077A
; Publication No. US20030150009A1
; GENERAL INFORMATION:

```
; APPLICANT: Gallie, Daniel R.
; APPLICANT: Young, Todd E.
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: Generation of Multiple Embryo Maize
; FILE REFERENCE: 023070-121500US
; CURRENT APPLICATION NUMBER: US/10/072,077A
; CURRENT FILING DATE: 2002-02-07
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 3183
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: promoter
; LOCATION: (1)..(3183)
; OTHER INFORMATION: senescence-associated gene 12-1 (SAG12-1) promoter
US-10-072-077A-1

Query Match          16.7%; Score 31.2; DB 16; Length 3183;
Best Local Similarity 52.3%; Pred. No. 11;
Matches 69; Conservative 0; Mismatches 63; Indels 0; Gaps 0;

QY 5 TCCTGATCGATTGCAAACTACCTCCAAACCAACCCAGCTTTGTATCTGCTTACTGTGAT 64
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 404 TCATATATTGAGTATGATCTCACTAATAATCAATCACTATTCACCTGTTTCATTAAA 345

QY 65 CACCAAAAGTTGCTGATACGATGCGAATATGCTCTTTCTCTTAGAAGTTCTCTG 124
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 344 AAAACAAGTTTCGTATATATAAACTTGGAATATGTTTAAATTAATTGAACGTACATT 285

QY 125 CCGATGCTTTAT 136
    ||| ||| |||
Db 284 GTTATGGGTCT 273

RESULT 9
US-10-437-963-71135/c
; Sequence 71135, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 71135
; LENGTH: 1852
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_71638C.1
US-10-437-963-71135

Query Match          16.6%; Score 31; DB 18; Length 1852;
Best Local Similarity 59.8%; Pred. No. 9.9;
Matches 52; Conservative 0; Mismatches 35; Indels 0; Gaps 0;

QY 15 ATTGCAATCTACCTCCAAACCAACCCAGCTTTGTATCTGCTTACTGTGATCAACCAAGTT 74
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 946 ATTGCTAGTCCCTCTCCCAAGCAATCTCTCTTTCTCTCTTCTGATGGCATCAACATCGTT 887

QY 75 GTGCTGATACGATGTCGGAATTATTGCT 101
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
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Db 886 GTTATCAGCACCTACACCACTTCTTGGT 860

RESULT 10
US-10-489-062-1
; Sequence 1, Application US/10489062
; Publication No. US20050055738A1
; GENERAL INFORMATION:
; APPLICANT: The University of North Carolina at Chapel Hill
; APPLICANT: Dangl, Jeffrey L
; APPLICANT: Epple, Petra
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR REGULATION OF CELL DEATH IN PLANTS
; FILE REFERENCE: 421/50 PCT
; CURRENT APPLICATION NUMBER: US/10/489,062
; CURRENT FILING DATE: 2004-03-09
; PRIOR APPLICATION NUMBER: US 60/326,534
; PRIOR FILING DATE: 2001-09-28
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 3000
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (766)..(843)
; OTHER INFORMATION:
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (2020)..(2130)
; OTHER INFORMATION:
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (2276)..(2311)
; OTHER INFORMATION:
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1366)..(1476)
; OTHER INFORMATION:
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1153)..(1278)
; OTHER INFORMATION:
US-10-489-062-1

Query Match          16.5%; Score 30.8; DB 19; Length 3000;
Best Local Similarity 54.4%; Pred. No. 14;
Matches 62; Conservative 0; Mismatches 52; Indels 0; Gaps 0;

QY 10 GATCGATTGCAAACTACCTCCAAACCAACCCAGCTTTGTATCTGCTTACTGTGATCACA 69
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2157 GATCGGTTTTAAATCAGTCGCAAACTAACAAAATTACTTCTCTTTTTTTTAAACATCAG 2216

QY 70 AAGTTGTGCTGATACGATGTCGGAATTATTGCTCTTTCTCTCTAGAAATGTTCT 123
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2217 AACGTTCTTTATATATGTTTATTTTGGTCTGCTATTGTTGATAATTGCT 2270

RESULT 11
US-10-741-600-17653/c
; Sequence 17653, Application US/10741600
; Publication No. US20050026169A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001499
; CURRENT APPLICATION NUMBER: US/10/741,600
; CURRENT FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 73997
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17653
; LENGTH: 39105
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; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(39105)
; OTHER INFORMATION: n = A,T,C or G, or insertion/deletion polymorphism (see Tables 1-
US-10-741-600-17653

Query Match      16.5%; Score 30.8; DB 19; Length 39105;
Best Local Similarity 48.3%; Pred. No. 41;
Matches 86; Conservative 0; Mismatches 92; Indels 0; Gaps 0;

Qy 10 GATCGATTGCAATCTACCTCCCAACCAACCCAGCTTTGTATCTCTTACTGTGATCAACA 69
Db 916 GGTAGGTTACAGACATGGGTTTGTCTTAGCAATGTATCTTCAAGGTTTGAACACAT 857

Qy 70 AAGTTGTGCTGATACGATGTCGATTATTGCTCTTCTCTAGATGTTCTCTGCGCAT 129
Db 856 AAGTTTGAAGTTTGTGTTAGGATGCTACATTCGCCAGTTGATCTCCCTGGAGTC 797

Qy 130 GCTTTATPAGAGAAGTTGTCAGCATCGATCTCTGCCAGTGTCTAGCTGAGAACATG 187
Db 796 CCTGAGAGAAGGTCAGTGGGAGCAAAATGGGSCCTTTGTAGGGGTGGGCGAGGAACATG 739

RESULT 12
US-10-424-599-128315/c
; Sequence 128315, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 128315
; LENGTH: 2723
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_86874C.1
US-10-424-599-128315

Query Match      16.3%; Score 30.4; DB 17; Length 2723;
Best Local Similarity 51.5%; Pred. No. 19;
Matches 70; Conservative 0; Mismatches 66; Indels 0; Gaps 0;

Qy 44 TTGTATCTGCTTACTGTGATCACCAGTTGTGCTGATAGATGTCGGATTATTGCTCT 103
Db 798 TATCAACAGCAGCAATTGTGTAATAGAAGTCGTTCTGCTGCGAGTGCATCTTTTGTCTC 739

Qy 104 TTCTTCTCTAGATGTTCTCCCGATGCTTTATAGAGAAGTTGGTCAGCATCGATCTC 163
Db 738 CAAAATGGAAATGTTCTCTCGTATGATGGCAACATAAATTTCACTGATCAACTT 679

Qy 164 TGCCAGTGTCTAGCTG 179
Db 678 CAGAAGTAGCTTTCCG 663

RESULT 13
US-10-357-930-60121/c
; Sequence 60121, Application US/10357930
; Publication No. US20040259086A1
; GENERAL INFORMATION:
; APPLICANT: Schlegel, Robert
; APPLICANT: Endege, Wilson
; APPLICANT: Monahan, John
```

```
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF
; TITLE OF INVENTION: HUMAN PROSTATE CANCER
; FILE REFERENCE: MRI-007BCN
; CURRENT APPLICATION NUMBER: US/10/357,930
; CURRENT FILING DATE: 2003-02-04
; PRIOR APPLICATION NUMBER: 09/785,276
; PRIOR FILING DATE: 2003-02-16
; PRIOR APPLICATION NUMBER: 60/183,319
; PRIOR FILING DATE: 2000-02-17
; PRIOR APPLICATION NUMBER: 60/189,862
; PRIOR FILING DATE: 2000-03-16
; PRIOR APPLICATION NUMBER: 60/207,454
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: 60/211,314
; PRIOR FILING DATE: 2000-06-09
; PRIOR APPLICATION NUMBER: 60/219,007
; PRIOR FILING DATE: 2000-07-18
; PRIOR APPLICATION NUMBER: 60/255,281
; PRIOR FILING DATE: 2000-12-13
; NUMBER OF SEQ ID NOS: 62232
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 60121
; LENGTH: 311
; TYPE: DNA
; ORGANISM: Homo sapiens
; ORGANISM: Homo sapiens
US-10-357-930-60121

Query Match      16.1%; Score 30.2; DB 18; Length 311;
Best Local Similarity 62.7%; Pred. No. 8.9;
Matches 47; Conservative 0; Mismatches 28; Indels 0; Gaps 0;

Qy 109 CTCTAGAATGTTCTGCGCATGCTTTTATAAGAGAAGTTGTCAGCATCGATCTCTGCCA 168
Db 124 CTCTAGAATTTTAATGCTTTATATTTTATGTCAGTGTGTAGGCAACACATCTCTGCCA 65

Qy 169 GTGCTAGCTAGAGAA 183
Db 64 GTTCTGCTGAAAA 50

RESULT 14
US-10-741-600-17623/c
; Sequence 17623, Application US/10741600
; Publication No. US20050026169A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; FILE OF INVENTION: MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CU001499
; CURRENT APPLICATION NUMBER: US/10/741,600
; CURRENT FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 73997
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17623
; LENGTH: 93513
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(93513)
; OTHER INFORMATION: n = A,T,C or G, or insertion/deletion polymorphism (see Tables 1-
US-10-741-600-17623

Query Match      16.1%; Score 30.2; DB 19; Length 93513;
Best Local Similarity 52.0%; Pred. No. 93;
Matches 91; Conservative 0; Mismatches 83; Indels 1; Gaps 1;

Qy 14 GATTGCAATCTACCTCCCAACCAACCCAGCTTTGTATCTGCTTACTGTGATCACCAGT 73
Db 5357 GAATGCAAGACTGAACACAGAAACCTTAATTTGGAGCCCTCGACGAATAAGTAGAGA 5298

Qy 74 TGTGCTGATAGATGTGCGATTATTGCTCTTTCTT-CTCTAGAAATGTTCTGCGCATGCT 132
```

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Db      5297 TAGGATAATCCAGGGGAGTATTCTCTTTCTTGAAGAGAATGGTGCTACCATTCAT 5238
QY      133 TTATAAGAGAGAGTTGGTCAGCATCGATCTCTGCCAGTGTCTAGCTGAGAACATG 187
Db      5237 GGAGAAAAAAACACTCAGAAATGAAGTTATATGCATGTATGTGTGCATGCAGATG 5183
```

RESULT 15

```
US-10-461-862-136/c
; Sequence 136, Application US/10461862
; Publication No. US20050090434A1
; GENERAL INFORMATION:
; APPLICANT: David W. Morris
; APPLICANT: Marc S. Malandro
; TITLE OF INVENTION: Novel Therapeutic Targets in Cancer
; FILE REFERENCE: 529452001800
; CURRENT APPLICATION NUMBER: US/10/461,862
; CURRENT FILING DATE: 2003-06-13
; NUMBER OF SEQ ID NOS: 184
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 136
; LENGTH: 98345
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-461-862-136
```

```
Query Match      16.1%; Score 30.2; DB 19; Length 98345;
Best Local Similarity 53.9%; Pred. No. 95;
Matches 62; Conservative 0; Mismatches 53; Indels 0; Gaps 0;

QY      68 CAAAGTTGTGTGATACGATGCGAATTATGCTCTTTCTTCTCTAGAAATGTTCTGCGG 127
Db      36511 CCAGTAGCTCCAGAGTTTCTGCCAATGCTGTGTCCTTCTTCCCTCTCAGGTGCAAGACG 36452

QY      128 ATGCTTTTATAAGAGAAGGTTGGTCAGCATCTGCGCAGTGTCTAGCTGAGA 182
Db      36451 ATTGATTATGAGCAGAGAGGTTCCAGCTGAGCCTTCAGCCATAGCCAGCTAACA 36397
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Search completed: May 22, 2005, 16:22:00
Job time : 309.299 secs

Result No.	Score	Query		DB	ID	Description
		Match	Length			
1	33.4	17.9	2013	4	US-09-134-000C-1201	Sequence 1201, Ap
2	32.8	17.5	268449	4	US-09-949-016-17244	Sequence 17244, A
c 3	31.6	16.9	64638	4	US-09-949-016-11767	Sequence 11767, A
4	31.6	16.9	64639	4	US-09-949-016-13520	Sequence 13520, A
c 5	31.2	16.7	3182	3	US-08-971-395-1	Sequence 1, Appli
6	31.2	16.7	3183	1	US-08-413-135-1	Sequence 1, Appli
c 7	31	16.6	78125	4	US-09-949-016-16006	Sequence 16006, A
8	30.8	16.5	7960	4	US-09-949-016-14930	Sequence 14930, A
9	30.6	16.4	85122	4	US-09-949-016-14693	Sequence 14693, A
10	30.6	16.4	119214	4	US-09-949-016-12507	Sequence 12507, A
c 11	30.2	16.1	601	4	US-09-949-016-53012	Sequence 53012, A
c 12	30.2	16.1	81681	4	US-09-949-016-13274	Sequence 13274, A
c 13	29.8	15.9	7212	4	US-09-576-594-243	Sequence 243, App
c 14	29.6	15.8	150597	4	US-09-949-016-15379	Sequence 15379, A
c 15	29.2	15.6	699	4	US-09-328-352-3148	Sequence 3148, Ap
c 16	29.2	15.6	3348	3	US-09-302-620B-94	Sequence 94, Appl
17	29.2	15.6	3348	4	US-09-912-161-12	Sequence 12, Appl
c 18	29	15.5	714	4	US-09-134-000C-3372	Sequence 3372, Ap
c 19	28.8	15.4	966	4	US-09-328-352-1604	Sequence 1604, A
20	28.8	15.4	60141	4	US-09-949-016-15874	Sequence 15874, A
c 21	28.8	15.4	129899	4	US-09-949-016-14684	Sequence 14684, A
c 22	28.8	15.4	148156	4	US-09-949-016-11776	Sequence 11776, A
c 23	28.6	15.3	601	4	US-09-949-016-182913	Sequence 182913, A
24	28.6	15.3	601	4	US-09-949-016-182914	Sequence 182914, A
25	28.6	15.3	601	4	US-09-949-016-182915	Sequence 182915, A
c 26	28.6	15.3	51967	4	US-09-949-016-16982	Sequence 16982, A
c 27	28.6	15.3	56665	4	US-09-949-016-14026	Sequence 14026, A

;; PRIOR FILING DATE: 2000-10-20
;; PRIOR APPLICATION NUMBER: 60/237,768
;; PRIOR FILING DATE: 2000-10-03
;; PRIOR APPLICATION NUMBER: 60/231,498
;; PRIOR FILING DATE: 2000-09-08
;; NUMBER OF SEQ ID NOS: 207012
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 17244
;; LENGTH: 268449
;; TYPE: DNA
;; ORGANISM: Human
;; FEATURE:
;; NAME/KEY: misc feature
;; LOCATION: (1)-(268449)
;; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-17244

Query Match 17.5%; Score 32.8; DB 4; Length 268449;
Best Local Similarity 59.8%; Pred. No. 3.1;
Matches 55; Conservative 0; Mismatches 37; Indels 0; Gaps 0;

QY 73 TTGTCGTATAGATGCGATATATGCTCTTCTCTAGATGTTCTCCCGATGCT 132
DB 92262 TTATCTGATAGATTCTCAATATATTTCTGTGTTATCTTGAATTTGTTGACCTTCT 92321
QY 133 TTATAAGAGAAGTTGGTCAGCATGATCTCT 164
DB 92322 CAACAATATTTTGAATTCTGTCTATCTCT 92353

RESULT 3
US-09-949-016-11767/c
;; Sequence 11767, Application US/09949016
;; Patent No. 6812339
;; GENERAL INFORMATION:
;; APPLICANT: VENTER, J. Craig et al.
;; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;; FILE REFERENCE: CL001307
;; CURRENT APPLICATION NUMBER: US/09/949,016
;; CURRENT FILING DATE: 2000-04-14
;; PRIOR APPLICATION NUMBER: 60/241,755
;; PRIOR FILING DATE: 2000-10-20
;; PRIOR APPLICATION NUMBER: 60/237,768
;; PRIOR FILING DATE: 2000-10-03
;; PRIOR APPLICATION NUMBER: 60/231,498
;; PRIOR FILING DATE: 2000-09-08
;; NUMBER OF SEQ ID NOS: 207012
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 11767
;; LENGTH: 64638
;; TYPE: DNA
;; ORGANISM: Human
;; FEATURE:
;; NAME/KEY: misc feature
;; LOCATION: (1)-(64638)
;; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-11767

Query Match 16.9%; Score 31.6; DB 4; Length 64638;
Best Local Similarity 65.7%; Pred. No. 4.5;
Matches 46; Conservative 0; Mismatches 24; Indels 0; Gaps 0;

QY 46 TGTATCTGCTTACTGTGATCACCAGTTGGCTGTGATGATGCGATGATTTGCTCTTT 105
DB 47673 TATATAAGATTAAATGAGCAGTGAAGTTTGTCTAAGACATTCAGCTTTTATCTCTTC 47614
QY 106 CTCTCTAGA 115
DB 47613 ATTCTCTAAA 47604

RESULT 4

US-09-949-016-13520/c
;; Sequence 13520, Application US/09949016
;; Patent No. 6812339
;; GENERAL INFORMATION:
;; APPLICANT: VENTER, J. Craig et al.
;; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;; FILE REFERENCE: CL001307
;; CURRENT APPLICATION NUMBER: US/09/949,016
;; CURRENT FILING DATE: 2000-04-14
;; PRIOR APPLICATION NUMBER: 60/241,755
;; PRIOR FILING DATE: 2000-10-20
;; PRIOR APPLICATION NUMBER: 60/237,768
;; PRIOR FILING DATE: 2000-10-03
;; PRIOR APPLICATION NUMBER: 60/231,498
;; PRIOR FILING DATE: 2000-09-08
;; NUMBER OF SEQ ID NOS: 207012
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 13520
;; LENGTH: 64639
;; TYPE: DNA
;; ORGANISM: Human
;; FEATURE:
;; NAME/KEY: misc feature
;; LOCATION: (1)-(64639)
;; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-13520

Query Match 16.9%; Score 31.6; DB 4; Length 64639;
Best Local Similarity 65.7%; Pred. No. 4.5;
Matches 46; Conservative 0; Mismatches 24; Indels 0; Gaps 0;

QY 46 TGTATCTGCTTACTGTGATCACCAGTTGGCTGTGATGATGCGATGATTTGCTCTTT 105
DB 47673 TATATAAGATTAAATGAGCAGTGAAGTTTGTCTAAGACATTCAGCTTTTATCTCTTC 47614
QY 106 CTCTCTAGA 115
DB 47613 ATTCTCTAAA 47604

RESULT 5
US-08-971-395-1/c
;; Sequence 1, Application US/08971395
;; Patent No. 6359197
;; GENERAL INFORMATION:
;; APPLICANT: Amasino, Richard M
;; APPLICANT: No. 6359197, Yoo-Sun
;; APPLICANT: Gan, Susheng
;; TITLE OF INVENTION: Transgenic Plants with Altered
;; TITLE OF INVENTION: Senseless Characteristics
;; NUMBER OF SEQUENCES: 5
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Quarles & Brady
;; STREET: 1 South Pinckney Street
;; CITY: Madison
;; STATE: WI
;; COUNTRY: US
;; ZIP: 53701-2113
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/971,395
;; FILING DATE:
;; CLASSIFICATION: 800
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Seay, Nicholas J.
;; REGISTRATION NUMBER: 27386
;; REFERENCE/DOCKET NUMBER: 960296.94908
;; TELECOMMUNICATION INFORMATION:

TELEPHONE: 608-251-5000
TELEFAX: 608-251-9166
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3182 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-971-395-1

Query Match 16.7%; Score 31.2; DB 3; Length 3182;
Best Local Similarity 52.3%; Pred. No. 1.8;
Matches 69; Conservative 0; Mismatches 63; Indels 0; Gaps 0;

QY 5 TCTGGATCGATTGCAAACTACCTCCAAACCCAGCTTTGTATCTGCTTACTGTGAT 64
DB 404 TCATATATTGATGATTGATCTTAATTCATATCACTTCACTGTTTCATTAAA 345
QY 65 CACCAAGTTGTGCTGATACGATGCGATTGCTCTTTCTCTAGAAATGTTCTG 124
DB 344 AAAACAAGTTTCGTATATAAACTTGGAAATATTGTTTAAATTAATTGAACGTACATT 285
QY 125 CCGATGCTTTAT 136
DB 284 GTTATGGGTCT 273

RESULT 6
US-08-413-135-1/c
Sequence 1, Application US/08413135
Patent No. 5689042
GENERAL INFORMATION:
APPLICANT: Amasino, Richard M
APPLICANT: Gan, Sushang
TITLE OF INVENTION: Transgenic Plants with Altered
TITLE OF INVENTION: Senescence Characteristics
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Quarles & Brady
STREET: 1 South Pinckney Street
CITY: Madison
STATE: WI
COUNTRY: US
ZIP: 53703
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/413,135
FILING DATE:
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Seay, Nicholas J
REGISTRATION NUMBER: 27,386
REFERENCE/DOCKET NUMBER: 960296.92808
TELECOMMUNICATION INFORMATION:
TELEPHONE: 608-251-5000
TELEFAX: 608-251-9166
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3183 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "SAG12-1 Promoter DNA"
US-08-413-135-1

Query Match 16.7%; Score 31.2; DB 1; Length 3183;
Best Local Similarity 52.3%; Pred. No. 1.8;

Matches 69; Conservative 0; Mismatches 63; Indels 0; Gaps 0;
QY 5 TCTGGATCGATTGCAAACTACCTCCAAACCCAGCTTTGTATCTGCTTACTGTGAT 64
DB 404 TCATATATTGATGATTGATCTTAATTCATATCACTTCACTGTTTCATTAAA 345
QY 65 CACCAAGTTGTGCTGATACGATGCGATTGCTCTTTCTCTAGAAATGTTCTG 124
DB 344 AAAACAAGTTTCGTATATAAACTTGGAAATATTGTTTAAATTAATTGAACGTACATT 285
QY 125 CCGATGCTTTAT 136
DB 284 GTTATGGGTCT 273
RESULT 7
US-09-949-016-16006
Sequence 16006, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 16006
LENGTH: 78125
TYPE: DNA
ORGANISM: Human
US-09-949-016-16006

Query Match 16.6%; Score 31; DB 4; Length 78125;
Best Local Similarity 68.3%; Pred. No. 7.9;
Matches 43; Conservative 0; Mismatches 20; Indels 0; Gaps 0;
QY 106 CTTCTCTAGAAATGTTCTGCGATGCTTTTAAAGAGAGGTTGTCAGATCGATCTCTG 165
DB 77416 CTGCTTAGGCTGCTGCTGCTTAAAGAGAGGTTTCCAGAAATCAGATGG 77475
QY 166 CCA 168
DB 77476 ACA 77478

RESULT 8
US-09-949-016-14930
Sequence 14930, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 14930

Query Match 13.5%; Score 29.8; DB 4; Length 712;
Best Local Similarity 51.1%; Pred No 7 7.

; TYPE: DNA

LENGTH: 699
TYPE: DNA
ORGANISM: Acinetobacter baumannii

US-09-328-352-3148

Query Match	15.6%	Score 29.2;	DB 4;	Length 699;
Best Local Similarity	56.1%	Pred. No. 4.7;		
Matches	55;	Conservative 0;	Mismatches 43;	Indels 0; Gaps 0;

Qy	89	TGCGATTATTGCTCTTTCTCTCTAGAAATGTTCCCTGCCGATGCTTTATAAGAGAGAGGTTG	148
Db	576	TACAATAATTGAACGTTTTTTCATCGTCAGGTTTATGAACCTGTTTCATAAAAGAATGTCG	517

Qy	149	GTCAGCATCGATCTCTGCCAGTGTCTTAGCTGAGAACAT	186
Db	516	ATCTGATTGATTGTTAATAGTGACATTGTTCTTCTT	479

Search completed: May 22, 2005, 13:49:35
Job time : 76.11 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 22, 2005, 10:33:14 ; Search time 125.89 Seconds
(without alignments)
4185.250 Million cell updates/sec

Title: US-10-058-566-5
Perfect score: 322
Sequence: 1 gaattctgctcggcggtc.....agttctagtgagaacatg 322

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA.*
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3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	33.4	10.4	2013	US-09-134-000C-1201	Sequence 1201, Ap
2	32.8	10.2	268449	US-09-949-016-17244	Sequence 17244, A
3	32.4	10.1	4942	US-09-474-076-1	Sequence 1, Appli
4	32.4	10.1	6435	US-09-949-016-2884	Sequence 2884, Ap
5	32.4	10.1	6435	US-09-949-016-2885	Sequence 2885, Ap
6	32.4	10.1	6594	US-09-949-016-2990	Sequence 2990, Ap
7	32.4	10.1	6594	US-09-949-016-2991	Sequence 2991, Ap
8	32.4	10.1	21914	US-09-949-016-14626	Sequence 14626, A
9	32.4	10.1	21914	US-09-949-016-14627	Sequence 14627, A
10	32.4	10.1	21914	US-09-949-016-14732	Sequence 14732, A
11	32.4	10.1	21914	US-09-949-016-14733	Sequence 14733, A
12	32	9.9	3182	US-08-971-395-1	Sequence 1, Appli
13	32	9.9	3183	US-08-413-135-1	Sequence 1, Appli
14	31.8	9.9	1947	US-08-987-367-3	Sequence 3, Appli
15	31.6	9.8	64638	US-09-949-016-11767	Sequence 11767, A
16	31.6	9.8	64639	US-09-949-016-13520	Sequence 13520, A
17	31	9.6	1141	US-09-806-708B-22	Sequence 22, Appl
18	31	9.6	1753	US-09-436-699C-15	Sequence 15, Appl
19	31	9.6	2265	US-09-369-618-3	Sequence 3, Appli
20	31	9.6	2265	US-09-369-617-3	Sequence 3, Appli
21	31	9.6	78125	US-09-313-294A-16006	Sequence 16006, A
22	30.8	9.6	300	US-09-313-294A-5664	Sequence 5664, Ap
23	30.8	9.6	7960	US-09-949-016-14930	Sequence 14930, A
24	30.6	9.5	85122	US-09-949-016-14693	Sequence 14693, A
25	30.6	9.5	119214	US-09-949-016-12507	Sequence 12507, A
26	30.2	9.4	601	US-09-949-016-53012	Sequence 53012, A
27	30.2	9.4	81681	US-09-949-016-13274	Sequence 13274, A

ALIGNMENTS

RESULT 1

US-09-134-000C-1201
; Sequence 1201, Application US/09134000C
; Patent No. 6617156
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; FILE REFERENCE: ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 032796-032
; CURRENT APPLICATION NUMBER: US/09/134.000C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/055,778
; PRIOR FILING DATE: 1997-08-15
; NUMBER OF SEQ ID NOS: 6812
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1201
; LENGTH: 2013
; TYPE: DNA
; ORGANISM: Enterococcus faecalis
US-09-134-000C-1201

Query Match	10.4%	Score 33.4;	DB 4;	Length 2013;
Best Local Similarity	52.5%	Pred. No. 0.38;		
Matches	73;	Conservative	0;	Mismatches 66; Indels 0; Gaps 0;
Qy	143	GGATCGATTGCAATCTACCTCAACCAACCCAGCTTTGTATCTGTTACTGTGATCAC	202	
Db	1698	TGGAACGATTGTACACTATTCCCAACAAACATGATAGTTGATTTTCAGATAACGG	1757	
Qy	203	CAAGTTGTCTGATGATGCGATATGCTTTCTTCTCTAGATGTTCTGCGC	262	
Db	1758	CACAGATTATTGATTCATATTGGATTGTACAGTTCAATTAGAACGCGAAGCTTTGA	1817	
Qy	263	ATGCTTTTATAAGAGAAGGT	281	
Db	1818	AGCTTTTGTAAACACAGGT	1836	

RESULT 2

US-09-949-016-17244
; Sequence 17244, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755

```
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17244
; LENGTH: 268449
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)-(268449)
; OTHER INFORMATION: n = A,T,C or G
;
US-09-949-016-17244

Query Match          10.2%; Score 32.8; DB 4; Length 268449;
Best Local Similarity 59.8%; Pred. No. 7.5;
Matches 55; Conservative 0; Mismatches 37; Indels 0; Gaps 0;

QY 208 TTGTGCTGATACGATGCGATTATGCTCTTTCTCTAGAAATGTTCTCGCCGATGCT 267
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 92262 TTATCTGATAGATTCTCAATTAATTTCTGTGTTATCTTGAAATTTGTTGACCTTCT 92321

QY 268 TTATAGAGAAGTTGTCAGCATCGATCTCT 299
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 92322 CAACAATTTATTTGAATTTCTGTCTATCTCT 92353

RESULT 3
US-09-474-076-1
; Sequence 1, Application US/09474076
; Patent No. 6465237
; GENERAL INFORMATION:
; APPLICANT: Tomlinson, James E.
; TITLE OF INVENTION: CLONING AND CHARACTERIZATION OF A HUMAN ADENYLYL
; TITLE OF INVENTION: CYCLASE
; FILE REFERENCE: 44481-5028-01-US
; CURRENT APPLICATION NUMBER: US/09/474,076
; CURRENT FILING DATE: 1999-12-12
; PRIOR APPLICATION NUMBER: PCT/US98/13694
; PRIOR FILING DATE: 1998-07-01
; PRIOR APPLICATION NUMBER: 60/070,904
; PRIOR FILING DATE: 1997-07-01
; PRIOR APPLICATION NUMBER: 08/886,550
; PRIOR FILING DATE: 1997-07-01
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 4942
; TYPE: DNA
; ORGANISM: human type VI adenylyl cyclase
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (145)..(3648)
;
US-09-474-076-1

Query Match          10.1%; Score 32.4; DB 3; Length 4942;
Best Local Similarity 49.4%; Pred. No. 1.4;
Matches 84; Conservative 0; Mismatches 86; Indels 0; Gaps 0;

QY 86 AATGGCGCAGTCGCTACTTATCACACCAACTTATCACCTAGAAAAGCGCGTCCTGG 145
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 4559 AAGGGGCGATGGAGCATCTCTTCTCTGTTGCCAAATAGAAAAGGTCAGGGCATGG 4618

QY 146 ATCGATTGCAATCTACCTCCACCAACCCAGCTTGTATCTGCTTACTGTGATCACCA 205
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 4619 AGAAGGTGACCTGTATGCCAAACCTGCCCTCCCAAGTCTCTGTTGGAGGGCCCG 4678

QY 206 AGTTGTGCTGATACGATGTCGATTATTGCTCTTTCTCTAGAAATGTT 255
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 5070 TGTGTTTGTGTAAGTGTGTCATGTTGGTCTTTTGTGTCATATCTGTT 5119

Query Match          10.1%; Score 32.4; DB 4; Length 6435;
Best Local Similarity 49.4%; Pred. No. 1.6;
Matches 84; Conservative 0; Mismatches 86; Indels 0; Gaps 0;

QY 86 AATGGCGCAGTCGCTACTTATCACCAACTTATCACCTAGAAAAGCGCGTCCTGG 145
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 4950 AAGGGGCGATGGAGCATCTCTTCTCTTCTGTTGCCAAATAGAAAAGGTCAGGGCATGG 5009

QY 146 ATCGATTGCAATCTACCTCCAAACCCAGCTTGTATCTGCTTACTGTGATCACCAA 205
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 5010 AGAAGGTGACCTGTATGCCAAACCTGCCCTCCCAAGTCTCTGTTGGAGGGCCCG 5069

QY 206 AGTTGTGCTGATACGATGTCGATTATTGCTCTTTCTCTAGAAATGTT 255
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 5070 TGTGTTTGTGTAAGTGTGTCATGTTGGTCTTTTGTGTCATATCTGTT 5119

RESULT 5
US-09-949-016-2885
; Sequence 2885, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2885
; LENGTH: 6435
; TYPE: DNA
; ORGANISM: Human
;
US-09-949-016-2885

Query Match          10.1%; Score 32.4; DB 4; Length 6435;
Best Local Similarity 49.4%; Pred. No. 1.6;
Matches 84; Conservative 0; Mismatches 86; Indels 0; Gaps 0;

Db 4679 TGTGTTTGTGTAAGTGTGTCATGTTGGTCTTTTGTGTCATATCTGTT 4728

RESULT 4
US-09-949-016-2884
; Sequence 2884, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2884
; LENGTH: 6435
; TYPE: DNA
; ORGANISM: Human
;
US-09-949-016-2884
```



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;
;
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Quarles & Brady
; STREET: 1 South Pinckney Street
; CITY: Madison
; STATE: WI
; COUNTRY: US
; ZIP: 53701-2113
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/971,395
; FILING DATE:
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Seay, Nicholas J.
; REGISTRATION NUMBER: 27386
; REFERENCE/DOCKET NUMBER: 960296.94908
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 608-251-5000
; TELEFAX: 608-251-9166
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3182 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; DESCRIPTION: /desc = "SAG12-1 Promoter DNA"
; US-08-413-135-1

Query Match          9.9%; Score 32; DB 3; Length 3182;
Best Local Similarity 50.7%; Pred. No. 1.5;
Matches 77; Conservative 0; Mismatches 75; Indels 0; Gaps 0;

Qy 120 TCACCTAGAAAGCGAGCGCTCTGGATTCGAAATCTCAACCAACCCAGCT 179
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Db 424 TCATATATACATCATTCATATATGAGTATTCATTAATTCATATCAACT 365

Qy 180 TTGTATCTGCTTACTGTGATCACCAGAGTTGTCTGATACGATGCGATTGCTCTT 239
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 364 ATTCAACTGTTTCATTAAAAAACAAGTTTCGTATATAAACTTGGAAATATTGTTTT 305

Qy 240 TCCTCTAGAAATGTTCTCGCGATGCTTTAT 271
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Db 304 AATTAATTGAACGTACATTTGTTATGGTTCT 273

RESULT 13
US-08-413-135-1/c
; Sequence 1, Application US/08413135
; Patent No. 5689042
; GENERAL INFORMATION:
; APPLICANT: Amasino, Richard M
; APPLICANT: Gan, Sushang
; TITLE OF INVENTION: Transgenic Plants with Altered
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Quarles & Brady
; STREET: 1 South Pinckney Street
; CITY: Madison
; STATE: WI
; COUNTRY: US
; ZIP: 53703
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:

; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Quarles & Brady
; STREET: 1 South Pinckney Street
; CITY: Madison
; STATE: WI
; COUNTRY: US
; ZIP: 53701-2113
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/971,395
; FILING DATE:
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Seay, Nicholas J.
; REGISTRATION NUMBER: 27386
; REFERENCE/DOCKET NUMBER: 960296.94908
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 608-251-5000
; TELEFAX: 608-251-9166
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3182 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; DESCRIPTION: /desc = "SAG12-1 Promoter DNA"
; US-08-413-135-1

Query Match          9.9%; Score 32; DB 3; Length 3182;
Best Local Similarity 50.7%; Pred. No. 1.5;
Matches 77; Conservative 0; Mismatches 75; Indels 0; Gaps 0;

Qy 120 TCACCTAGAAAGCGAGCGCTCTGGATTCGAAATCTCAACCAACCCAGCT 179
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Db 424 TCATATATACATCATTCATATATGAGTATTCATTAATTCATATCAACT 365

Qy 180 TTGTATCTGCTTACTGTGATCACCAGAGTTGTCTGATACGATGCGATTGCTCTT 239
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 364 ATTCAACTGTTTCATTAAAAAACAAGTTTCGTATATAAACTTGGAAATATTGTTTT 305

Qy 240 TCCTCTAGAAATGTTCTCGCGATGCTTTAT 271
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Db 304 AATTAATTGAACGTACATTTGTTATGGTTCT 273

RESULT 14
US-08-987-367-3/c
; Sequence 3, Application US/08987367
; Patent No. 6399859
; GENERAL INFORMATION:
; APPLICANT: Nichols, Scott
; APPLICANT: Dhugga, Kanwarpal S.
; APPLICANT: Singletary, George William
; APPLICANT: Saunders, Court
; APPLICANT: Witcher, Derrick
; APPLICANT: Bruce, Wesley B.
; APPLICANT: Sims, Lynne
; APPLICANT: Lu, Guihua
; APPLICANT: Zhong, Gan-Yuan
; TITLE OF INVENTION: PLANT URIDINE DIPHOSPHATE-GLUCOSE
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/987,367
; FILING DATE: 10-DEC-1997
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Jones, Phil B.C.
; REGISTRATION NUMBER: 38,195
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; REFERENCE/DOCKET NUMBER: 750027.404
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 822-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1947 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-987-367-3

Query Match          9.9%; Score 31.8; DB 3; Length 1947;
Best Local Similarity 67.2%; Pred. No. 1.4;
Matches 45; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

QY 14 GCGGTTCAACTGAACCGTAAACAGTGGAAAGTGGATCTCTTTCTCTCTGCAATCCGT 73
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Db 113 GCGGTTCAACCGCACCCACCGACGGAGAGAGAGAGGAGCGGCGATCTCTCTGCTTCCTT 54
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QY 74 GCGGTGG 80
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Db 53 GCGCGG 47

RESULT 15
US-09-949-016-11767/c
; Sequence 11767, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11767
; LENGTH: 64638
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(64638)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-11767

Query Match          9.8%; Score 31.6; DB 4; Length 64638;
Best Local Similarity 65.7%; Pred. No. 9.6;
Matches 46; Conservative 0; Mismatches 24; Indels 0; Gaps 0;

QY 181 TGTATCTGCTTACTGTGATCACCAGAGTTGCTGTGATGATGCGATTATTGCTCTTT 240
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Db 47673 TATATAAGATTAAATGAGCAGTGTGCTGTGATGATGCGATTATTGCTCTTT 240
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QY 241 CTTCTCTAGA 250
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Db 47613 ATTCTCTAAA 47604
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Search completed: May 22, 2005, 13:49:32
 Job time : 130.89 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: May 22, 2005, 13:22:20 ; Search time 525.701 Seconds
(without alignments)
3756.139 Million cell updates/sec

Title: US-10-058-566-5

Perfect score: 322

Sequence: 1 gaattctcgtcgtcggtc.....agtgtctagtgagaacatg 322

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 5695437 seqs, 3066160638 residues

Total number of hits satisfying chosen parameters: 11390874

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*
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- 17: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq:*
- 18: /cgn2_6/ptodata/1/pubpna/US10F_PUBCOMB.seq:*
- 19: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
- 20: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq:*
- 21: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
- 22: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	322	100.0	322	13	US-10-058-566-5
2	322	100.0	2544	13	US-10-058-566-3
3	187	58.1	187	13	US-10-058-566-6
4	44.2	13.7	714	17	US-10-260-238-2894
5	33.4	10.4	9797	9	US-09-070-927A-550
6	33	10.2	88576	17	US-10-085-117-319
7	32.6	10.1	1601042	13	US-10-027-632-59064
8	32.6	10.1	1601042	17	US-10-027-632-59064
9	32.4	10.1	533	17	US-10-424-599-77478
10	32.4	10.1	1411	17	US-10-424-599-104812
11	32.4	10.1	4942	13	US-10-201-000-1

12	32.4	10.1	6440	18	US-10-719-993-266	Sequence 266, App
13	32.4	10.1	6594	19	US-10-887-553A-116	Sequence 116, App
14	32.4	10.1	6599	18	US-10-719-993-267	Sequence 267, App
15	32.4	10.1	29921	18	US-10-719-993-6848	Sequence 6848, App
16	32	9.9	3183	16	US-10-072-0778A-1	Sequence 1, Appli
17	31.8	9.9	243	18	US-10-425-115-6855	Sequence 6855, Ap
18	31.8	9.9	285	9	US-09-294-093B-5286	Sequence 5286, Ap
19	31.8	9.9	394	18	US-10-425-115-160956	Sequence 160956, A
20	31.8	9.9	1861	17	US-10-425-114-24318	Sequence 24318, A
21	31.8	9.9	1947	17	US-10-097-691-3	Sequence 3, Appli
22	31.8	9.9	2617	18	US-10-425-115-151022	Sequence 151022, A
23	31.8	9.9	94917	13	US-10-087-192-184	Sequence 184, App
24	31.6	9.8	1047	17	US-10-369-493-42137	Sequence 42137, A
25	31.6	9.8	352938	18	US-10-322-696-79	Sequence 79, Appli
26	31.4	9.8	39105	19	US-10-741-600-17653	Sequence 17653, A
27	31.2	9.7	1411	17	US-10-425-114-23051	Sequence 23051, A
28	31.2	9.7	1420	18	US-10-425-115-100941	Sequence 100941, A
29	31	9.6	1753	17	US-10-454-199-15	Sequence 15, Appli
30	31	9.6	1852	18	US-10-437-963-71135	Sequence 71135, A
31	30.8	9.6	3000	19	US-10-489-062-1	Sequence 1, Appli
32	30.8	9.6	29963	19	US-10-741-600-17858	Sequence 17858, A
33	30.8	9.6	86893	19	US-10-741-600-17773	Sequence 17773, A
34	30.6	9.5	479	18	US-10-653-047-3483	Sequence 3483, Ap
35	30.6	9.5	637	13	US-10-027-632-189544	Sequence 189544, A
36	30.6	9.5	637	17	US-10-027-632-189544	Sequence 189544, A
37	30.4	9.4	2723	17	US-10-424-599-128315	Sequence 128315, A
38	30.2	9.4	311	18	US-10-357-930-60121	Sequence 60121, A
39	30.2	9.4	664	18	US-10-425-115-4800	Sequence 4800, Ap
40	30.2	9.4	1648	18	US-10-425-115-166128	Sequence 166128, A
41	30.2	9.4	1650	18	US-10-739-930-2202	Sequence 2202, Ap
42	30.2	9.4	1683	18	US-10-425-115-151019	Sequence 151019, A
43	30.2	9.4	1952	18	US-10-425-115-151016	Sequence 151016, A
44	30.2	9.4	7221	9	US-09-764-855-234	Sequence 234, App
45	30.2	9.4	7221	14	US-10-072-349-234	Sequence 234, App

ALIGNMENTS

RESULT 1
US-10-058-566-5
; Sequence 5, Application US/10058566
; Publication No. US20020183274A1
; GENERAL INFORMATION:
; APPLICANT: ALBERTSEN, MARC
; APPLICANT: FOX, TIM
; APPLICANT: HUFFMAN, GARY
; APPLICANT: TRIMNELL, MARY
; TITLE OF INVENTION: NUCLEOTIDE SEQUENCES MEDIATING MALE FERTILITY AND
; FILE REFERENCE: PHI 1147
; CURRENT APPLICATION NUMBER: US/10/058,566
; CURRENT FILING DATE: 2002-01-28
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 322
; TYPE: DNA
; ORGANISM: Zea mays
US-10-058-566-5

Query Match 100.0%; Score 322; DB 13; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.1e-100;
Matches 322; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	GAATTCCTCGTCTCGCGGTCAACTGAACCGTAAACAGTGAAGTGGATATCTTTCTCT 60
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Qy	61	CTCTGCAATCGTCCCGTGGAGCAATGGCGAGTCGCTTACTATCACACCACTTAT 120
Db	61	CTCTGCAATCGTCCCGTGGAGCAATGGCGAGTCGCTTACTATCACACCACTTAT 120

QY 121 CACCTAGAAAAGCGAGCGCTCTGGATCGATTGCAAACTACCTCCAAACCAACCCAGCTT 180
DB 121 CACCTAGAAAAGCGAGCGCTCTGGATCGATTGCAAACTACCTCCAAACCAACCCAGCTT 180
QY 181 TGTATCTGCTTACTGTGATCACCAGAAAGTTGTCTGATACGATGTGCGATTATTGCTCTTT 240
DB 181 TGTATCTGCTTACTGTGATCACCAGAAAGTTGTCTGATACGATGTGCGATTATTGCTCTTT 240
QY 241 CTTCTCTAGAAATGTTCTCTCCGATGCTTTTATAAGAGAAGTTGGTCAGCATCGATCTCTG 300
DB 241 CTTCTCTAGAAATGTTCTCTCCGATGCTTTTATAAGAGAAGTTGGTCAGCATCGATCTCTG 300
QY 301 CCAGTGTCTAGCTGAGAACATG 322
DB 301 CCAGTGTCTAGCTGAGAACATG 322

RESULT 2

US-10-058-566-3
; Sequence 3, Application US/10058566
; Publication No. US20020183274A1
; GENERAL INFORMATION:
; APPLICANT: ALBERTSEN, MARC
; APPLICANT: FOX, TIM
; APPLICANT: HUFFMAN, GARY
; APPLICANT: TRIMMELL, MARY
; TITLE OF INVENTION: NUCLEOTIDE SEQUENCES MEDIATING MALE FERTILITY AND
; FILE REFERENCE: PHI 1147
; CURRENT APPLICATION NUMBER: US/10/058,566
; CURRENT FILING DATE: 2002-01-28
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 2544
; TYPE: DNA
; ORGANISM: Zea mays
US-10-058-566-3

Query Match 100.0%; Score 322; DB 13; Length 2544;
Best Local Similarity 100.0%; Pred. No. 1.6e-99;
Matches 322; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GAATTCCTCTCGGCGGTCACCTGAACCGTAAACAGTGGAAAGTGGATCTCTTCTCT 60
DB 1 GAATTCCTCTCGGCGGTCACCTGAACCGTAAACAGTGGAAAGTGGATCTCTTCTCT 60
QY 61 CTCTGCAATCCGTCGCGTGGAGCAAAATGGCGCAGTGGCTTACTTATCACACCACTTAT 120
DB 61 CTCTGCAATCCGTCGCGTGGAGCAAAATGGCGCAGTGGCTTACTTATCACACCACTTAT 120
QY 121 CACCTAGAAAAGCGAGCGCTCTGGATCGATTGCAAACTACCTCCAAACCAACCCAGCTT 180
DB 121 CACCTAGAAAAGCGAGCGCTCTGGATCGATTGCAAACTACCTCCAAACCAACCCAGCTT 180
QY 181 TGTATCTGCTTACTGTGATCACCAGAAAGTTGTCTGATACGATGTGCGATTATTGCTCTTT 240
DB 181 TGTATCTGCTTACTGTGATCACCAGAAAGTTGTCTGATACGATGTGCGATTATTGCTCTTT 240
QY 241 CTTCTCTAGAAATGTTCTCTCCGATGCTTTTATAAGAGAAGTTGGTCAGCATCGATCTCTG 300
DB 241 CTTCTCTAGAAATGTTCTCTCCGATGCTTTTATAAGAGAAGTTGGTCAGCATCGATCTCTG 300
QY 301 CCAGTGTCTAGCTGAGAACATG 322
DB 301 CCAGTGTCTAGCTGAGAACATG 322

RESULT 3

US-10-058-566-6
; Sequence 6, Application US/10058566
; Publication No. US20020183274A1
; GENERAL INFORMATION:

; APPLICANT: ALBERTSEN, MARC
; APPLICANT: FOX, TIM
; APPLICANT: HUFFMAN, GARY
; APPLICANT: TRIMMELL, MARY
; TITLE OF INVENTION: NUCLEOTIDE SEQUENCES MEDIATING MALE FERTILITY AND
; FILE REFERENCE: PHI 1147
; CURRENT APPLICATION NUMBER: US/10/058,566
; CURRENT FILING DATE: 2002-01-28
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 187
; TYPE: DNA
; ORGANISM: Zea mays
US-10-058-566-6

Query Match 58.1%; Score 187; DB 13; Length 187;
Best Local Similarity 100.0%; Pred. No. 1.2e-53;
Matches 187; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 1 CGGTCCTCGATCGATTGCAAACTACCTCCAAACCAACCCAGCTTGTGATCTGCTTACTG 60
QY 196 TGTATCCAAAGTTGTCTGATACGATGTGCGATTATTGCTCTTCTCTCTAGAAATGTT 255
DB 61 TGTATCCAAAGTTGTCTGATACGATGTGCGATTATTGCTCTTCTCTCTAGAAATGTT 120
QY 256 CTGCGCGATGCTTTATAAGAGAAGTTGGTCAGCATCGATCTCTGCGAGTGTCTAGCTGA 315
DB 121 CTGCGCGATGCTTTATAAGAGAAGTTGGTCAGCATCGATCTCTGCGAGTGTCTAGCTGA 180
QY 316 GAACATG 322
DB 181 GAACATG 187

RESULT 4

US-10-260-238-2894
; Sequence 2894, Application US/10260238
; Publication No. US20040016025A1
; GENERAL INFORMATION:
; APPLICANT: Budworth, Paul R.
; APPLICANT: Moughamer, Todd G.
; APPLICANT: Briggs, Steven P.
; APPLICANT: Cooper, Bret
; APPLICANT: Glazebrook, Jane
; APPLICANT: Goff, Stephen A.
; APPLICANT: Katagiri, Fumiyaki
; APPLICANT: Kreps, Joel
; APPLICANT: Provart, Nicholas
; APPLICANT: Ricke, Darrell
; APPLICANT: Zhu, Tong
; TITLE OF INVENTION: PROMOTERS FOR REGULATION OF PLANT EXPRESSION
; FILE REFERENCE: 60111-NP
; CURRENT APPLICATION NUMBER: US/10/260,238
; CURRENT FILING DATE: 2002-09-26
; PRIOR APPLICATION NUMBER: US 60/325,448
; PRIOR FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: US 60/325,277
; PRIOR FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: US 60/370,620
; PRIOR FILING DATE: 2002-04-04
; NUMBER OF SEQ ID NOS: 6077
; SEQ ID NO 2894
; LENGTH: 714
; TYPE: DNA
; ORGANISM: Triticum aestivum
US-10-260-238-2894
Query Match 13.7%; Score 44.2; DB 17; Length 714;
Best Local Similarity 61.3%; Pred. No. 0.00029;

```
Matches 106; Conservative 0; Mismatches 63; Indels 4; Gaps 2;
QY 122 ACTAGAAAGCAGCGCTCTGGATGATGCAATCTACCTCCAAACCCAGCTTT 181
Db 414 ACCTGTACCTAGATCTTCAAGATGACTGTAAATCTGCATCTTACCAACCCAGCTTT 473
QY 182 GTATCTGCTTACTGTATGATACCAAGTTGCTGATACGATGCGATTTATCTCTTTC 241
Db 474 GTACCTGTTAAATGCTGTATGATCAAAAATGGGG---TGAAGAACCATCTTGTATCTCC 530
QY 242 TTCTCTAGAAATGTTCTCTGCGATGCTTTTATAAGAGAAGTTGCTGACGATCGA 294
Db 531 TCCTCTAGATGTTCTTTCAGCTGC-TTATATGAGAAGCTGGATTTGGCTCAA 582

RESULT 5
US-09-070-927A-550/c
; Sequence 550, Application US/09070927A
; Patent No. US20020120116A1
; GENERAL INFORMATION:
; APPLICANT: Charles A. Kunsch
; Patrick J. Dillon
; Steven Batash
; TITLE OF INVENTION: Enterococcus faecialis Polynucleotides and Polypeptides
; NUMBER OF SEQUENCES: 982
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.44Mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/070,927A
; FILING DATE: 04-May-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/046,655
; FILING DATE: 1997-05-16
; APPLICATION NUMBER: 60/044,031
; FILING DATE: 1997-05-06
; APPLICATION NUMBER: 60/066,009
; FILING DATE: 1997-11-14
; ATTORNEY/AGENT INFORMATION:
; NAME: Kenley K. Hoover
; REGISTRATION NUMBER: 40,302
; REFERENCE/DOCKET NUMBER: PB369
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 550:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9797 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 550:
US-09-070-927A-550

Query Match 10.4%; Score 33.4; DB 9; Length 9797;
Best Local Similarity 52.5%; Pred. No. 5;
Matches 73; Conservative 0; Mismatches 66; Indels 0; Gaps 0;
QY 143 TGGATGATTCGAATCTACCTCCAAACCCAGCTTTGATCTGCTTACTGTGATCAC 202
Db 4260 TGGAACGATTTGCACACTATTTCCCAACAAACATGATAGTTTGTATTCAGATACGG 4201
QY 203 CAAAGTTGTGCTGATACGATGCGGATTTATGCTCTTTCTCTAGAAATGTTCTCTCGCG 262
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Db 4200 CACAGAAATTTATGATTCATATTTGGGATTCATACAGTTCAATTAGAAGCGAAGGCTTTGA 4141
QY 263 ATGCTTTTATAAGAGAAGGT 281
Db 4140 AGCTTTTGTAAACCAAGGT 4122

RESULT 6
US-10-085-117-319
; Sequence 319, Application US/10085117
; Publication No. US20030232334A1
; GENERAL INFORMATION:
; APPLICANT: Morris, David W.
; APPLICANT: Engelhard, Eric K.
; TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR CANCER
; FILE REFERENCE: 529452000121
; CURRENT APPLICATION NUMBER: US/10/085,117
; CURRENT FILING DATE: 2002-02-27
; PRIOR APPLICATION NUMBER: US 09/798,586
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 361
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 319
; LENGTH: 88576
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: variation
; LOCATION: (1)...(88576)
; OTHER INFORMATION: n = any nucleotide
US-10-085-117-319

Query Match 10.2%; Score 33; DB 17; Length 88576;
Best Local Similarity 49.7%; Pred. No. 19;
Matches 84; Conservative 0; Mismatches 85; Indels 0; Gaps 0;
QY 43 AGTGGATACTCTTCTCTCTGCAATCCGTGCGGTGGAGCAAAATGGCGCAGTCGCCTA 102
Db 51848 AATCAATACTCTTAATCTCTGAGCCATCCCTCCAGTCCCAATCATATGATGATTTAAACATT 51907
QY 103 CTTATCACACCAACTTATCATTACCTAGAAAAGCAGCGGTCTCGATTCATTCGAAATCTAC 162
Db 51908 CTTTATAGAAACAGCAGCAGCTGAGGGGGCCACACAGCTCATGTGCGTTTCATGTCA 51967
QY 163 CTCCAACCAACCCAGCTTTGTATCTGCTTACTGTGATTCACCAAGTTGT 211
Db 51968 CCCCAGCCACGTAATGTGTGTACTTCTTGTGTTCCCATTAATTTTT 52016
```

```
RESULT 7
US-10-027-632-59064
; Sequence 59064, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; POLYMORPHISMS IN THE HUMAN GENOME
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
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; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 59064
; LENGTH: 1601042
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(1601042)
; OTHER INFORMATION: n = A,T,C or G
US-10-027-632-59064

Query Match 10.1%; Score 32.6; DB 13; Length 1601042;
Best Local Similarity 53.7%; Pred. No. 98;
Matches 66; Conservative 1; Mismatches 56; Indels 0; Gaps 0;

QY 6 CTCGCTCGCGGTCAACTGAACCGTAAACAGTGGAAAGTGATCTCTTCTCTCTG 65
DB 444322 CCTTCAACACAGATGCCGAAACCTTATGAAGCTGAATTAGATCTCTTCCCTACCTC 444381

QY 66 CAATCGTCCGCTGGAAGCAATGGCGCAGTCGCCTACTTATCACACCAACTTATCACT 125
DB 444382 ATTCGCDGTCCGCGACCACTGTAACACCATCTGGATAGCGCTCAGACAGCCCTATCATCA 444441

QY 126 AGA 128
DB 444442 ACA 444444

RESULT 8

US-10-027-632-59064
; Sequence 59064, Application US/10027632
; Publication No. US20030204075A9

; GENERAL INFORMATION:
; APPLICANT: Wang, David G.

; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide

; FILE REFERENCE: Polymorphisms in the Human Genome

; CURRENT APPLICATION NUMBER: US/10/027,632

; CURRENT FILING DATE: 2002-04-30

; PRIOR APPLICATION NUMBER: US 60/218,006

; PRIOR FILING DATE: 2000-07-12

; PRIOR APPLICATION NUMBER: US 60/198,676

; PRIOR FILING DATE: 2000-04-20

; PRIOR APPLICATION NUMBER: US 60/193,483

; PRIOR FILING DATE: 2000-03-29

; PRIOR APPLICATION NUMBER: US 60/185,218

; PRIOR FILING DATE: 2000-02-24

; PRIOR APPLICATION NUMBER: US 60/167,363

; PRIOR FILING DATE: 1999-11-23

; PRIOR APPLICATION NUMBER: US 60/156,358

; PRIOR FILING DATE: 1999-09-28

; PRIOR APPLICATION NUMBER: US 60/146,002

; PRIOR FILING DATE: 1999-08-09

; NUMBER OF SEQ ID NOS: 325720

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 59064

; LENGTH: 1601042

; TYPE: DNA

; ORGANISM: Human

; FEATURE:
; NAME/KEY: misc_feature

; LOCATION: (1)...(1601042)

; OTHER INFORMATION: n = A,T,C or G

US-10-027-632-59064

Query Match 10.1%; Score 32.6; DB 17; Length 1601042;
Best Local Similarity 53.7%; Pred. No. 98;
Matches 66; Conservative 1; Mismatches 56; Indels 0; Gaps 0;

QY 6 CTCGCTCGCGGTCAACTGAACCGTAAACAGTGGAAAGTGATCTCTTCTCTCTG 65

DB 444322 CCTTCAACACAGATGCCGAAACCTTATGAAGCTGAATTAGATCTCTTCCCTACCTC 444381

QY 66 CAATCGTCCGCTGGAAGCAAAATGGCGCAGTCGCCTACTTATCACACCAACTTATCACT 125
DB 444382 ATTCGCDGTCCGCGACCACTGTAACACCATCTGGATAGCGCTCAGACAGCCCTATCATCA 444441

QY 126 AGA 128
DB 444442 ACA 444444

RESULT 9

US-10-424-599-77478

; Sequence 77478, Application US/10424599

; Publication No. US20040031072A1

; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J

; APPLICANT: Kovalic David K

; APPLICANT: Zhou Yihua

; APPLICANT: Cao Yongwei

; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With

; FILE REFERENCE: Plants and Uses Thereof for Plant Improvement

; CURRENT APPLICATION NUMBER: US/10/424,599

; CURRENT FILING DATE: 2003-04-28

; NUMBER OF SEQ ID NOS: 285684

; SEQ ID NO 77478

; LENGTH: 533

; TYPE: DNA

; ORGANISM: Glycine max

; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_40980C.1

US-10-424-599-77478

Query Match

Best Local Similarity 10.1%; Score 32.4; DB 17; Length 533;

Matches 66; Conservative 0; Mismatches 56; Indels 0; Gaps 0;

QY 159 CTACCTCAACCAACCCAGCTTTGTATCTGTCTTACTGTGATCACCAAGTTGTCTGATA 218

DB 253 CTGCTTCATCTTCCCATCATCTCTCATGCCCTCGAATGGGATTCACCTGGCTGATT 312

QY 219 CGATGTGGGATTATTGCTCTTCTCTAGAAATGTTCTGCCGATGCTTTTATAAGAGAA 278

DB 313 TCGTCATGCCCTTTTCTTTTCATGCTGGAATTTCTCTGCCCCCTCGTTTATAAGAGAA 372

QY 279 GG 280

DB 373 GG 374

RESULT 10

US-10-424-599-104812

; Sequence 104812, Application US/10424599

; Publication No. US20040031072A1

; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J

; APPLICANT: Kovalic David K

; APPLICANT: Zhou Yihua

; APPLICANT: Cao Yongwei

; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With

; FILE REFERENCE: Plants and Uses Thereof for Plant Improvement

; CURRENT APPLICATION NUMBER: US/10/424,599

; CURRENT FILING DATE: 2003-04-28

; NUMBER OF SEQ ID NOS: 285684

; SEQ ID NO 104812

; LENGTH: 1411

; TYPE: DNA

; ORGANISM: Glycine max

; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_65661C.1


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; FILE REFERENCE: CL001496
; CURRENT APPLICATION NUMBER: US/10/719,993
; CURRENT FILING DATE: 2003-11-24
; NUMBER OF SEQ ID NOS: 55342
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 267
; LENGTH: 6599
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-719-993-267

Query Match      10.1%; Score 32.4; DB 18; Length 6599;
Best Local Similarity 49.4%; Pred. No. 9.1;
Matches 84; Conservative 0; Mismatches 86; Indels 0; Gaps 0;

QY 86 ATGGCGCAGTCGCCCTACTTATCACACCAACCCAGCTTTGTATCTGCTTACTGTGATCACCAC 205
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 5110 AAGGGGCGATGGAGCATCTCTCTCTCTGTTGCCAAATAGAAAAGGTCAGGGCATGG 5169

QY 146 ATCGATTGCAATCTACCTCCACCAACCCAGCTTTGTATCTGCTTACTGTGATCACCAC 205
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 5170 AGAAGGTGACCTGATGCCAACCTGCCCTCCCAAGTCTCTGGTGTGGGAGGGCCCG 5229

QY 206 AGTTGTGCTGATACGATGCGGATTATGCTCTTTCTTCTCTAGAAATGTT 255
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 5230 TGTGTTTGTAAGTGTGTGTCATGTTGGTCTTTGTGTGCATATCTGTT 5279

RESULT 15
US-10-719-993-6848
; Sequence 6848, Application US/10719993
; Publication No. US20040265849A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: ALZHEIMER'S DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001496
; CURRENT APPLICATION NUMBER: US/10/719,993
; CURRENT FILING DATE: 2003-11-24
; NUMBER OF SEQ ID NOS: 55342
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6848
; LENGTH: 29921
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(29921)
; OTHER INFORMATION: n = A,T,C or G, or insertion/deletion polymorphism (see Tables 1-
US-10-719-993-6848

Query Match      10.1%; Score 32.4; DB 18; Length 29921;
Best Local Similarity 49.4%; Pred. No. 18;
Matches 84; Conservative 0; Mismatches 86; Indels 0; Gaps 0;

QY 86 ATGGCGCAGTCGCCCTACTTATCACACCAACCTTATCACCTAGAAAAGCAGCGTCTCTGG 145
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 22433 AAGGGGCGATGGAGCATCTCTCTCTGTTGCCAAATAGAAAAGGTCAGGGCATGG 22492

QY 146 ATCGATTGCAAACTACCTCCACCAACCCAGCTTTGTATCTGCTTACTGTGATCACCAC 205
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 22493 AGAAGGTGACCTGATCCCAACCTGCCCTCCCAAGTCTCTGGTGTGGGAGGGCCCG 22552

QY 206 AGTTGTGCTGATACGATGCGGATTATGCTCTTTCTTCTCTAGAAATGTT 255
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 22553 TGTGTTTGTAAGTGTGTGTCATGTTGGTCTTTGTGTGCATATCTGTT 22602

Search completed: May 22, 2005, 16:21:56
Job time : 533.701 secs
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